

# **EXHIBIT**

**2**

## CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQIDNO1 488 aa

Sequence 2: SEQIDNO3. 488 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 96

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-2

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:10380

Alignment Score 2880

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-200



## CLUSTAL W (1.82) multiple sequence alignment

```

SEQIDNO1      KEIAVTIDDKNVIASVSESFHGVAFDASLFSPKGLWSPKLFKLLLEGLSPGYFRV 60
SEQIDNO3      KEIAVTIDDKNVIASASGSFLGVAFDASLFSPKGLWSFVDITSPKLFKLLLEGLSPGYFRV 60
*****
SEQIDNO1      GGTGANWLFDDLNNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETEDDLVKLTG 120
SEQIDNO3      GGTGANWLFDDLNNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDNLVKLTG 120
*****
SEQIDNO1      SKMRLFLDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS 180
SEQIDNO3      SKMRLFLDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS 180
*****
SEQIDNO1      AHNLTEKQVGEDFKALHKVLEKYPTLNKGS LVGPDVGWGMVSVYVKGLADGAGDLVTAFTL 240
SEQIDNO3      AHNLTEKQVGEDFKALHKVLEKYPTLNKGS LVGPDVGWGMVSVXVKGLADEAGDHVTAFTL 240
*****
SEQIDNO1      HQYYFDGNTSDVSTYLDATYFKKLQQLFDKVKDVLKNSQHKDKPLWLGETSSGYNSGTD 300
SEQIDNO3      HQYYFDGNTSDVSIYLDATYFKKLQQLFDKVKDVLKDSPHKDEPLWLGETSSGYNSGTED 300
*****
SEQIDNO1      VSDRYVSGFLTLDKLGLSAANNVKVIRQTIYNGYYGLLDKNTLEPNPDYWL MHVHNSLV 360
SEQIDNO3      VSDRYVSGFLTLDKLGLSAANNVKVIRQTIYNGYYGLLDKNTLEPNPDYWL MHVHNSLV 360
*****
SEQIDNO1      GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGS LTIFALNVGDEDVTLKIDQYGG 420
SEQIDNO3      GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGS LTIFALNVGDGDVTLKIGQYSG 420
*****
SEQIDNO1      KKIYSYILTPEGGQLTSQKVLLNGKELKLVSDQLPELNANESKTSFTLSPKTFGFFVVS 480
SEQIDNO3      KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVVS 480
*****
SEQIDNO1      ANVEACKK 488
SEQIDNO3      ANVEACKK 488
*****

```



## CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQIDNO3 488 aa

Sequence 2: SEQIDNO5 488 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 97

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-2

Start of Multiple Alignment

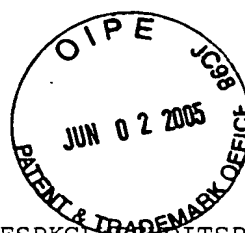
There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:10465

Alignment Score 2927

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-200



## CLUSTAL W (1.82) multiple sequence alignment

```

SEQIDNO3      KEIAVTIDDKNVIASASGSFLGVAFDASLFSPKGLWAFDITSPKLFKLLLEGLSPGYFRV  60
SEQIDNO5      KEIAVTIDDKNVIASASESFHGVAFDASLFSPKGLWSFVDITSPKLFKLLLEGLSPGYFRV  60
*****

SEQIDNO3      GGTGANWLFDDLNNKWKDYWAFKDKTPETATITRRWLFKQNNLKKETFDNLVKLTG  120
SEQIDNO5      GGTGANWLFDDLNNKWKDYWAFKDKTPETATITRRWLFKQNNLKKETFDNLVKLTG  120
*****

SEQIDNO3      SKMRLFLDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNPDHTS  180
SEQIDNO5      SKMRLFLDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNPDHTS  180
*****

SEQIDNO3      AHNLTEKQVGEDFKALHKVLEKYPTLNKGSVLGPDVGWGMGVSXVKGLADEAGDHVTAFTL  240
SEQIDNO5      AHNLTEKQVGEDFKALHKVLEKYPTLNKGSVLGPDVGWGMGVSXVKGLADEAGDHVTAFTL  240
*****

SEQIDNO3      HQYYFDGNTSDVSIYLDATYFKKLQQLFDKVKDVLKDSPHKDEPLWLGETSSGYNSGTED  300
SEQIDNO5      HQYYFDGNTSDVSIYLDATYFKKLQQLFDKVKDVLKDSPHKDKPLWLGETSSGYNSGTED  300
*****

SEQIDNO3      VSDRYVSGFLTLDKLGLSAANNVKVVIROTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV  360
SEQIDNO5      VSDRYVSGFLTLDKLGLSAANNVKVVIROTIYSGYYGPLDKNTLEPNPDYWLMHVHNSLV  360
*****

SEQIDNO3      GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDGDVTLKIGQYSG  420
SEQIDNO5      GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDEDVTLKIGQYSG  420
*****

SEQIDNO3      KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVSD  480
SEQIDNO5      KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPQLNADESKTSFTLSPKTFGFFVSD  480
*****

SEQIDNO3      ANVEACKK 488
SEQIDNO5      ANVEACKK 488
*****

```



## CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQIDNO3 488 aa

Sequence 2: SEQIDNO7 488 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 94

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-2

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:10323

Alignment Score 2848

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-200



## CLUSTAL W (1.82) multiple sequence alignment

```

SEQIDNO3      KEIAVTIDDKNVIASASGSFLGVAFDASLFSPKGLWSFVDITSPKLFKLLLEGLSPGYFRV 60
SEQIDNO7      KEIAVTIDDKNVIASVSESFHGVAFDASLFSPKGPWSFVNITSPKLFKLLLEGLSPGYFRV 60
*****
*****

SEQIDNO3      GGTGANWLFDDLNNKWKDYWAFKDKTPETATITRRWLFKQNNLKKETFDNLVKLTKG 120
SEQIDNO7      GGTGANWLFDDLNNKWKDYWAFKDKTPETATITRRWLFKQNNLKKETFDNLVKLTKG 120
*****
*****

SEQIDNO3      SKMRLFLDLNAEVRTGYEIGKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS 180
SEQIDNO7      SKMRLFLDLNAEVRTGYEIGKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS 180
*****
*****

SEQIDNO3      AHNLTEKQVGEDFKALHKVLEKYPTLNKGSVGPVGMVSVXVKGLADEAGDHVTAFTL 240
SEQIDNO7      AHNLTEKQVGEDFKALHKVLEKYPTLNKGSVGPVGMVSVYVKGLADGAGDLVTAFTL 240
*****
*****

SEQIDNO3      HQYYFDGNTSDVSIYLDATYFKKLQQLFDKVKDVLKDSPHKDEPLWLGETSSGYNSTGTE 300
SEQIDNO7      HQYYFDGNTSDVSTYLDASYFKKLQQLFDKVKDVLKNSPHKDKPLWLGETSSGCNSGTGD 300
*****
*****

SEQIDNO3      VSDRYVSGFLTLDKLGLSAANNVKVVIROTIYNGYYGLLDKNTLEPNPDYWLMLHVHNSLV 360
SEQIDNO7      VSDRYVSGFLTLDKLGLSAANNVKVVIROTIYNGYYGLLDKNTLEPNPDYWLMLHVHNSLV 360
*****
*****

SEQIDNO3      GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSALTIFALNVGDGDVTLKIGQYSG 420
SEQIDNO7      GNTVFKVDVSDPTNKTRVYAQCTKTNSKHTQGKYYKGSALTIFALNVGDEEVLTKIDQYGG 420
*****
*****

SEQIDNO3      KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVSD 480
SEQIDNO7      KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVSD 480
*****
*****

SEQIDNO3      ANVEACKK 488
SEQIDNO7      ANVEACKK 488
*****

```